



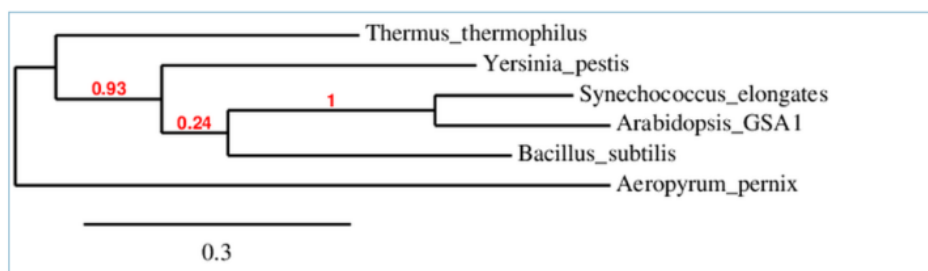
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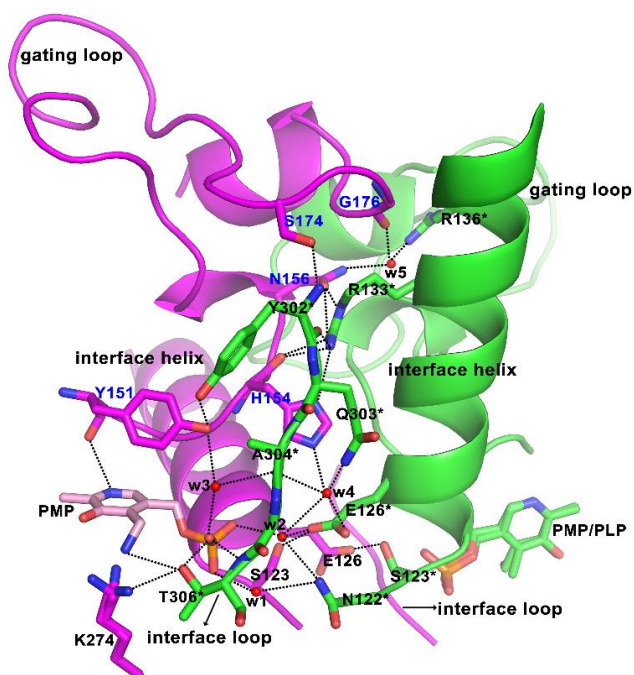
**Supporting information for article:**

**Crystal structure of glutamate-1-semialdehyde-2,1-aminomutase from  
*Arabidopsis thaliana***

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**Figure S1** Phylogenetic relationship of GSAM from *Arabidopsis thaliana*, *Synechococcus elongates*, *Bacillus subtilis*, *Yersinia pestis*, *Thermus thermophiles*, and *Aeropyrum pernix*. Bootstrap analyses were computed with 1,000 replicates, and the values of percentage are shown on the branches.



**Figure S2** A proposed model displaying hydrogen-bond network involved in the negative cooperativity between monomers of GSAM. Specifically, (i) cofactor and Lys274 send active-site information by interacting with the neighboring interface helix/loop through the following hydrogen bonds, cofactor-w1-Asn122\*, cofactor-w2-Glu126\*, cofactor-w3-Ala304\*, cofactor/Lys274-Thr306\*. (ii) Gating-loop (residues 151-184) information is transmitted through interactions with the neighboring interface helix/loop, i.e. Tyr151-Tyr302\*, His154-w4-Glu126\*/Gln303\*/Ala304\*, His154-Arg133\*, Asn156-Arg133\*, Asn156-w5-Arg136\*, Ser174-Tyr302\*, Gly176-w5-Arg136\*. (iii) Interface helices from the two monomers can interact

with each other (Ser123-Glu126\*, Glu126-Ser123\*). (iv) Besides, hydrogen-bond interactions also exist between cofactor and gating loop (cofactor-Tyr151), between interface helix and interface loop from the same monomer (Tyr302\*-Arg133\*, Gln303\*/Ala304\*-w4-Glu126\*), between interface loop and residues participating in substrate pocket lining (Ser30-Gly305\*, Arg33-Thr306\*) (data not shown). Subunit A and B of *AtGSA1* is shown in magenta and green, respectively. All water molecules (red spheres) shown are conserved in at least *Synechococcus* GSAM and *AtGSA1* structures. Hydrogen-bond interactions are depicted as dotted dashes. The \* indicates the residue from the neighboring subunit.